Identification of Biomarkers for Cartilage Damage in Osteoarthritis by RNA-Seq and Proteomic Analysis

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Osteoarthritis (OA) is the most common joint disease, with over 527 million patients worldwide reported in 2019. The diagnosis of OA is mainly based on clinical findings and imaging studies. Currently there is no laboratory test available for OA diagnosis, mainly due to the lack of OA-specific biomarkers.The purpose of this project was to identify biomarkers that can be used for the development of laboratory diagnostics for OA. To this end, RNA-seq analysis was performed on GSE114007, a dataset containing RNA-seq data of cartilage chondrocytes from 18 healthy individuals and 20 OA patients. The results were verified with proteomics data by reanalyzing a mass spectrometry dataset of synovial fluid from 10 OA patients. RNA-seq analysis revealed 697 upregulated genes and 793 down-regulated genes in chondrocytes from OA patients compared to healthy control individuals. Of particular interest, a panel of genes related to extracellular matrix, including lumican (LUM), tenascin C (TNC), fibronectin 1 (FN1), collagen 1a1(COL1A1), cartilage acidic protein 1 (CRTAC1), osteoglycin (OGN), and HtrA serine peptidase 1 (HTRA1), were significantly upregulated in OA patients. Proteins encoded by these genes were all detected in synovial fluid of OA, likely resulting from cartilage damage and chondrocyte breakdown. These genes and proteins may serve as OA-specific biomarkers that can be used to develop laboratory tests for OA diagnosis and disease follow-up, and may serve as potential drug targets for OA treatment as well.

Awards Won:

University of Texas at Dallas: Scholarship of $5,000 per year, renewable for up to four years